

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/633,452

DATE: 02/21/2001  
 TIME: 10:59:55

Input Set : A:\97-15C4.SEQ.txt  
 Output Set: N:\CRF3\02212001\I633452.raw

**ENTERED**

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Presnell, Scott R.  
 6 Gilbert, Teresa  
 C--> 8 (ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE-LIKE FACTOR-7  
 10 (iii) NUMBER OF SEQUENCES: 43  
 12 (iv) CORRESPONDENCE ADDRESS:  
 13 (A) ADDRESSEE: ZymoGenetics, Inc.  
 14 (B) STREET: 1201 Eastlake Avenue East  
 15 (C) CITY: Seattle  
 16 (D) STATE: WA  
 17 (E) COUNTRY: USA  
 18 (F) ZIP: 98102  
 20 (v) COMPUTER READABLE FORM:  
 21 (A) MEDIUM TYPE: Diskette  
 22 (B) COMPUTER: IBM Compatible  
 23 (C) OPERATING SYSTEM: DOS  
 24 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
 26 (vi) CURRENT APPLICATION DATA:  
 C--> 27 (A) APPLICATION NUMBER: US/09/633,452  
 C--> 28 (B) FILING DATE: 07-Aug-2000  
 29 (C) CLASSIFICATION:  
 31 (vii) PRIOR APPLICATION DATA:  
 32 (A) APPLICATION NUMBER:  
 33 (B) FILING DATE:  
 35 (viii) ATTORNEY/AGENT INFORMATION:  
 36 (A) NAME: Lunn, Paul G  
 37 (B) REGISTRATION NUMBER: 32,743  
 38 (C) REFERENCE/DOCKET NUMBER: 97-15  
 40 (ix) TELECOMMUNICATION INFORMATION:  
 41 (A) TELEPHONE: 206-442-6627  
 42 (B) TELEFAX: 206-442-6678  
 43 (C) TELEX:  
 45 (2) INFORMATION FOR SEQ ID NO: 1:  
 47 (i) SEQUENCE CHARACTERISTICS:  
 48 (A) LENGTH: 736 base pairs  
 49 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: single  
 51 (D) TOPOLOGY: linear  
 53 (ii) MOLECULE TYPE: cDNA  
 54 (ix) FEATURE:  
 56 (A) NAME/KEY: Coding Sequence  
 57 (B) LOCATION: 57...596  
 58 (D) OTHER INFORMATION:  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 62 GAATTCGGCA CGAGGAGGCG GGCAGCAGCT GCAGGCTGAC CTTGCAGCTT GGC GGA ATG 59  
 63 Met

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64                                     1
66 GAC TGG CCT CAC AAC CTG CTG TTT CTT CTT ACC ATT TCC ATC TTC CTG      107
67 Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe Leu
68           5                10                15
70 GGG CTG GGC CAG CCC AGG AGC CCC AAA AGC AAG AGG AAG GGG CAA GGG      155
71 Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln Gly
72           20                25                30
74 CGG CCT GGG CCC CTG GCC CCT GGC CCT CAC CAG GTG CCA CTG GAC CTG      203
75 Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu
76           35                40                45
78 GTG TCA CGG ATG AAA CCG TAT GCC CGC ATG GAG GAG TAT GAG AGG AAC      251
79 Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn
80           50                55                60                65
82 ATC GAG GAG ATG GTG GCC CAG CTG AGG AAC AGC TCA GAG CTG GCC CAG      299
83 Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln
84           70                75                80
86 AGA AAG TGT GAG GTC AAC TTG CAG CTG TGG ATG TCC AAC AAG AGG AGC      347
87 Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser
88           85                90                95
90 CTG TCT CCC TGG GGC TAC AGC ATC AAC CAC GAC CCC AGC CGT ATC CCC      395
91 Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro
92           100               105               110
94 GTG GAC CTG CCG GAG GCA CGG TGC CTG TGT CTG GGC TGT GTG AAC CCC      443
95 Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro
96           115               120               125
98 TTC ACC ATG CAG GAG GAC CGC AGC ATG GTG AGC GTG CCG GTG TTC AGC      491
99 Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser
100          130               135               140               145
102 CAG GTT CCT GTG CGC CGC CGC CTC TGC CCG CCA CCG CCC CGC ACA GGG      539
103 Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly
104           150               155               160
106 CCT TGC CGC CAG CGC GCA GTC ATG GAG ACC ATC GCT GTG GGC TGC ACC      587
107 Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr
108           165               170               175
110 TGC ATC TTC TGAATCACCT GGCCAGAAG CCAGGCCAGC AGCCCGAGAC CATCCTCCT      645
111 Cys Ile Phe
112           180
114 TGCACCTTTG TGCCAAGAAA GGCCTATGAA AAGTAAACAC TGACTTTTGA AAGCCAGAAA      705
115 AAAAAAAAAA AAAAAAATT CCTGCGGCCG C      736
117 (2) INFORMATION FOR SEQ ID NO: 2:
119   (i) SEQUENCE CHARACTERISTICS:
120       (A) LENGTH: 180 amino acids
121       (B) TYPE: amino acid
122       (C) STRANDEDNESS: single
123       (D) TOPOLOGY: linear
125   (ii) MOLECULE TYPE: protein
126       (v) FRAGMENT TYPE: internal
128   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
130 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe

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131 1          5          10          15
132 Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln
133          20          25          30
134 Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
135          35          40          45
136 Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Tyr Glu Arg
137          50          55          60
138 Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala
139          65          70          75          80
140 Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
141          85          90          95
142 Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
143          100         105         110
144 Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn
145          115         120         125
146 Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe
147          130         135         140
148 Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr
149          145         150         155         160
150 Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys
151          165         170         175
152 Thr Cys Ile Phe
153          180
155 (2) INFORMATION FOR SEQ ID NO: 3:
157   (i) SEQUENCE CHARACTERISTICS:
158       (A) LENGTH: 397 base pairs
159       (B) TYPE: nucleic acid
160       (C) STRANDEDNESS: single
161       (D) TOPOLOGY: linear
163   (ii) MOLECULE TYPE: Other
165   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
167 AGGCGGGCAN AGCTGCAGGC TGACCTTGCA GCTTGCGGGA ATGGACTGGC CTCACAACCT    60
168 GCTGTTTCTT CTTACCATT CCATCTTCCT GGGGCTGGGC AGCCAGGAGC CCCAAAAGCA    120
169 AGAGGAAGGG GCAAGGGCGG CCTGGGCCCN TGGCCTGGCC TCACCAGGTG CCACTGGACC    180
170 TGGTGTACAG GATGAAACCG TATGCCCGCA TGGAGGAGTA TGAGAGGAAC ATCGAGGAGA    240
171 TGGTGGCCCA GCTGAGGAAC AGCTCANAAG CTGGCCCAGA GAAAGTGTGA GGTCAACTTG    300
172 CAGCTGTGGA TGTCCAACAA GAAGGAGCCT GTCTCCCTTG GGGCTACAAG CATCAACCAC    360
173 CGACCCAGC CGTATCCCG TGGGACCTTG CCGGGAC    397
175 (2) INFORMATION FOR SEQ ID NO: 4:
177   (i) SEQUENCE CHARACTERISTICS:
178       (A) LENGTH: 18 base pairs
179       (B) TYPE: nucleic acid
180       (C) STRANDEDNESS: single
181       (D) TOPOLOGY: linear
183   (ii) MOLECULE TYPE: Other
184   (vii) IMMEDIATE SOURCE:
185       (B) CLONE: ZC13265
187   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189 TTACCATTTC CATCTTCC    18

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191 (2) INFORMATION FOR SEQ ID NO: 5:
193   (i) SEQUENCE CHARACTERISTICS:
194       (A) LENGTH: 18 base pairs
195       (B) TYPE: nucleic acid
196       (C) STRANDEDNESS: single
197       (D) TOPOLOGY: linear
199   (ii) MOLECULE TYPE: Other
200   (vii) IMMEDIATE SOURCE:
201       (B) CLONE: ZC13266
203   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
205   CCCTTCCTCT TGCTTTTG                                     18
207 (2) INFORMATION FOR SEQ ID NO: 6:
209   (i) SEQUENCE CHARACTERISTICS:
210       (A) LENGTH: 29 base pairs
211       (B) TYPE: nucleic acid
212       (C) STRANDEDNESS: single
213       (D) TOPOLOGY: linear
215   (ii) MOLECULE TYPE: Other
216   (vii) IMMEDIATE SOURCE:
217       (B) CLONE: ZC13326
219   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
221   CAAGGATCCC AGCCCAGGAG CCCCAAAAG                       29
223 (2) INFORMATION FOR SEQ ID NO: 7:
225   (i) SEQUENCE CHARACTERISTICS:
226       (A) LENGTH: 30 base pairs
227       (B) TYPE: nucleic acid
228       (C) STRANDEDNESS: single
229       (D) TOPOLOGY: linear
231   (ii) MOLECULE TYPE: Other
232   (vii) IMMEDIATE SOURCE:
233       (B) CLONE: ZC13330
235   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
237   GACCTCGAGT CAGAAGATGC AGGTGCAGCC                       30
239 (2) INFORMATION FOR SEQ ID NO: 8:
241   (i) SEQUENCE CHARACTERISTICS:
242       (A) LENGTH: 30 base pairs
243       (B) TYPE: nucleic acid
244       (C) STRANDEDNESS: single
245       (D) TOPOLOGY: linear
247   (ii) MOLECULE TYPE: Other
248   (vii) IMMEDIATE SOURCE:
249       (B) CLONE: ZC13325
251   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
253   GTCGAATTCA TGGACTGGCC TCACAACCTG                       30
255 (2) INFORMATION FOR SEQ ID NO: 9:
257   (i) SEQUENCE CHARACTERISTICS:
258       (A) LENGTH: 27 base pairs
259       (B) TYPE: nucleic acid
260       (C) STRANDEDNESS: single

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261      (D) TOPOLOGY: linear
263      (ii) MOLECULE TYPE: Other
264      (vii) IMMEDIATE SOURCE:
265      (B) CLONE: ZC13327
267      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
269      GAAGGATCCG AAGATGCAGG TGCAGCC
271 (2) INFORMATION FOR SEQ ID NO: 10:
273      (i) SEQUENCE CHARACTERISTICS:
274          (A) LENGTH: 10 amino acids
275          (B) TYPE: amino acid
276          (C) STRANDEDNESS: single
277          (D) TOPOLOGY: linear
279      (ii) MOLECULE TYPE: peptide
281      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
283      Asp Tyr Lys Asp Asp Asp Lys Gly Ser
284      1          5          10
286 (2) INFORMATION FOR SEQ ID NO: 11:
288      (i) SEQUENCE CHARACTERISTICS:
289          (A) LENGTH: 692 base pairs
290          (B) TYPE: nucleic acid
291          (C) STRANDEDNESS: single
292          (D) TOPOLOGY: linear
294      (ii) MOLECULE TYPE: cDNA
295      (ix) FEATURE:
297          (A) NAME/KEY: Coding Sequence
298          (B) LOCATION: 50...589
299          (D) OTHER INFORMATION:
301      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
303      GGGGTTCTG GCGGGTGGCA GCTGCGGGCC TGCCGCCTGA CTTGGTGGG ATG GAC TGG      58
304                                          Met Asp Trp
305                                          1
307      CCG CAC AGC CTG CTC TTC CTC CTG GCC ATC TCC ATC TTC CTG GCG CCA      106
308      Pro His Ser Leu Leu Phe Leu Leu Ala Ile Ser Ile Phe Leu Ala Pro
309      5          10          15
311      AGC CAC CCC CGG AAC ACC AAA GGC AAA AGA AAA GGG CAA GGG AGG CCC      154
312      Ser His Pro Arg Asn Thr Lys Gly Lys Arg Lys Gly Gln Gly Arg Pro
313      20          25          30          35
315      AGT CCC TTG GCC CCT GGG CCT CAT CAG GTG CCG CTG GAC CTG GTG TCT      202
316      Ser Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser
317      40          45          50
319      CGA GTA AAG CCC TAC GCT CGA ATG GAA GAG TAT GAG CGG AAC CTT GGG      250
320      Arg Val Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn Leu Gly
321      55          60          65
323      GAG ATG GTG GCC CAG CTG AGG AAC AGC TCC GAG CCA GCC AAG AAG AAA      298
324      Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Pro Ala Lys Lys Lys
325      70          75          80
327      TGT GAA GTC AAT CTA CAG CTG TGG TTG TCC AAC AAG AGG AGC CTG TCC      346
328      Cys Glu Val Asn Leu Gln Leu Trp Leu Ser Asn Lys Arg Ser Leu Ser
329      85          90          95

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VERIFICATION SUMMARY                      DATE: 02/21/2001  
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Input Set : A:\97-15C4.SEQ.txt  
Output Set: N:\CRF3\02212001\I633452.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:8 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]